CURRENT STATUS OF ALL CLAIMS

1. (Previously amended) A method of determining amino acid sequence of a polypeptide, comprising:

(a) constructing a graph from mass spectra of two or more differentially labeled polypeptides, said graph comprising a node with mass m, number of labels n, intensity i, and mass differential of labels d;

(b) creating a node corresponding to a paired signal having masses of about m and about m+nd,

(c) adding a labeled weighted directed edge to said graph between any two nodes corresponding to a mass of an amino acid, said labeled weighted directed edge combining properties of said paired signals, and

(d) assigning a satisfying amino acid to two or more of said labeled weighted directed edges, thereby determining said amino acid sequence .

2. (Currently amended) The method of claim 1 ~~further comprising~~, **wherein step (b) further comprises**:

[[(e)]] (i) creating a source node with total mass M, total number of labels N and fixed intensity Is; and

[[(f)]] (ii) creating a terminus node with mass 0, minimum number of labels n_0, and fixed intensity I_t**[[;]].**

3. (Currently amended) The method of claim 2, ~~further comprising~~ **wherein step (b) further comprises (iii)** selecting a path from the source node to the terminus node.

4. (Original) The method of claim 3, further comprising computing a priority score for each path through the graph.

5. (Original) The method of claim 1, wherein said differential label marks an internal amino acid residue.

6. (Original) The method of claim 1, wherein said differential label marks a terminal amino acid residue.

7. (Original) The method of claim 1, wherein said differential label marks a terminal and an internal amino acid residue.

8. (Original) The method of claim 1, wherein said differentially labeled polypeptides further comprise stable isotopic labels.

9. (Original) The method of claim 1, wherein said differentially labeled polypeptides further comprise heavy and light labeled isotopes selected from the group consisting of hydrogen, carbon, oxygen, nitrogen, sulfur and selenium.

10. (Original) The method of claim 1, wherein said differentially labeled polypeptides further comprise an unlabeled polypeptide and a labeled polypeptide.

11. (Original) The method of claim 1, wherein said polypeptide is labeled *in vivo* or *in vitro*.

12. (Original) The method of claim 1, wherein said mass spectra are obtained from a mass spectrometry database.

13. (Original) The method of claim 1, wherein said mass spectra are of low resolution.

14. (Original) The method of claim 1, further comprising masses of amino acid post-translational modifications.

15. (Original) The method of claim 1, further comprising adding complement node with mass M-m, and a number of labels $N-n+n_0$.

16. (Original) The method of claim 1, further comprising including multiple amino acid edges between nodes, said multiple amino acid edges characterizing a degenerate amino acid residue in said polypeptide sequence.

17. (Original) The method of claim 1, wherein steps a-c are repeated one or more times.

18. (Original) The method of claim 1, wherein steps a-c are performed by an automated process.

19. (Original) A method of determining an amino acid sequence of a polypeptide, comprising:

(a) differentially labeling two or more polypeptide mixtures, and

(b) determining an amino acid sequence of a polypeptide within said mixture using the method of claim 1.

20. (Original) The method of claim 19, wherein said differential label marks an internal amino acid residue.

21. (Original) The method of claim 19, wherein said differential label marks a terminal amino acid residue.

22. (Original) The method of claim 19, wherein said differential label marks a terminal and an internal amino acid residue.

23. (Original) The method of claim 19, wherein said differentially labeled polypeptides further comprise stable isotopic labels.

24. (Original) The method of claim 19, wherein said differentially labeled polypeptides further comprise heavy and light labeled isotopes selected from the group consisting of hydrogen, carbon, oxygen, nitrogen, sulfur and selenium.

25. (Original) The method of claim 19, wherein said differentially labeled polypeptides further comprise an unlabeled polypeptide and a labeled polypeptide.

26. (Original) The method of claim 19, wherein said polypeptide is labeled *in vivo* or *in vitro*.

27. (Original) The method of claim 19, wherein said mass spectra are obtained from a mass spectrometry database.

28. (Original) The method of claim 19, wherein said mass spectra are of low resolution.

29. (Original) The method of claim 19, further comprising separating components of said mixture.

Claims 30 to 55. Cancelled.